

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1238 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 64.  
Location/Qualifiers

FEATURES  
source

1. .173  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1253939"  
/db\_xref="taxon:9606"  
/clone="IMAGE:310525"  
/tissue\_type="senescent fibroblast"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares\_senescent\_fibroblasts\_NbHSF"  
/note="Vector: pT7T3D (Pharmacia) with a modified  
polylinker V-type; phagemid; Site\_1: Not I; Site\_2: Eco RI  
; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5'  
TGTTACCAATCTGAAGTGGGAGCGCGCATTTTTTTTTTTTTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo." 49 t

SE COUNT 43 a 33 c 48 g 49 t  
IGIN  
Query Match 100.0%; Score 15; DB 14; Length 173;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 TCCATGGTGCTCACT 15  
|||||  
93 TCCATGGTGCTCACT 107

RESULT 2  
W637280 232 bp mRNA linear EST 26-APR-2001  
OCUS bl56gll.w1 Blackshear/Soares normalized xenopus egg library Xenopus  
EFINITION laevis cDNA clone PBX0056G11 5', mRNA sequence.

CCESSION AW637280.1 GI:7394388  
ERSION  
EYWORDS  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 232)  
AUTHORS Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.,  
Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman  
J.W., Bonaldo,M.F. and Soares,M.B.  
TITLE The NIEHS Xenopus maternal EST project: interim analysis of the  
first 13,879 ESTs from unfertilized eggs  
Gene 267 (1), 71-87 (2001)

JOURNAL 21211403  
MEDLINE 11311557  
PUBMED  
COMMENT Contact: Perry J. Blackshear  
Office of Clinical Research and Laboratory of Signal Transduction  
National Institute of Environmental Health Sciences  
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,  
USA  
Tel: 919 541-4899  
Fax: 919 541-4571  
Email: black009@niehs.nih.gov  
This clone is available through Research Genetics, Inc., 2130 Memorial  
Way, Huntsville, AL 35901  
ay, no. 536-9016 ext. cDNA, fax 256-536-9016 att: cDNA, email

cdna@resgen.com  
DNA Sequencing and analyses performed by National Institutes of  
Health Intramural Sequencing Center (NISC).

PCR Primers  
FORWARD: TGTAACACGACGGCCAGT  
BACKWARD: CAGGAACACGTATGACC  
Plate: 0056 row: G column: 11  
Seq primer: T7 primer.  
Location/Qualifiers

FEATURES  
source

1. .232  
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/clone="PBX0056G11"  
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/cell\_type="unfertilized egg"  
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/lab\_host="DH10B"  
/clone\_lib="Blackshear/Soares normalized xenopus egg  
library"  
/note="Vector: pT7T3-Pac; Site\_1: EcoRI; Site\_2: NotI;  
polyA-selected mRNA was prepared from unfertilized Xenopus  
laevis eggs. The library was constructed in the vector  
pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and  
Soares, M.B. 'Normalization and subtraction: two  
approaches to facilitate gene discovery', Genome Research  
6:791-806, 1996. The first strand synthesis used a  
NotI-dT18 primer; double stranded cDNAs were ligated to  
EcoRI adapters, digested with NotI, and directionally  
cloned into the NotI and EcoRI-digested pT7T3-Pac vector.  
The library contained approximately 7.2 X 10<sup>5</sup>  
recombinants, with average insert sizes of 1-1.5 kb." 47 t

BASE COUNT 71 a 49 c 65 g 47 t  
ORIGIN  
Query Match 100.0%; Score 15; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
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Db 67 TCCATGGTGCTCACT 81

RESULT 3  
AA360512 268 bp mRNA linear EST 21-APR-1997  
LOCUS EST69742 T-cell lymphoma Homo sapiens cDNA 5' end similar to  
DEFINITION hereditary multiple exostoses gene 2 (EXT2), mRNA sequence.

ACCESSION AA360512.1 GI:2012902  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 268)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult  
C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White  
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-wai,C., Clayton,R.A.,  
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald  
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,  
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,  
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,  
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,  
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,  
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,  
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon



M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280  
7566098  
Other\_ESTs: THCl94116  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1. .268  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/db\_xref="taxon:9606"  
/cell\_type="T-lymphocyte"  
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FEATURES  
source

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Query Match 100.0%; Score 15; DB 9; Length 268;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
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Db 248 TCCATGGTGCTCACT 262

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LOCUS BE132222 269 bp mRNA linear EST 29-JUN-2000  
DEFINITION db43g01.y1 Blackshear/Soares normalized xenopus egg library xenopus laevis cDNA clone IMAGE:3301296 5', mRNA sequence.  
ACCESSION BE132222  
VERSION BE132222.1 GI:8579587  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.  
REFERENCE 1 (bases 1 to 269)  
AUTHORS Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.  
WashU Xenopus EST project, 1999  
Unpublished  
Contact: Sandy Clifton, Ph.D.  
WashU Xenopus EST project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: [info@image.llnl.gov](mailto:info@image.llnl.gov)

TITLE  
JOURNAL  
COMMENT

Seq primer: -40RP from Gibco  
High quality sequence stop: 268.  
Location/Qualifiers  
1. .269  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
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/clone="IMAGE:3301296"  
/sex="female"  
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/cell\_type="unfertilized egg"  
/dev\_stage="unfertilized egg"  
/lab\_host="DH10B"  
/clone\_lib="Blackshear/Soares normalized Xenopus egg library"

/note="Vector: pT7T3-Pac; Site\_1: EcoRI; Site\_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT7T3-Pac vector. The library contained approximately 7.2 x 10<sup>5</sup> recombinants, with average insert sizes of 1-1.5 kb."  
BASE COUNT 79 a 61 c 73 g 55 t 1 others  
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 269;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
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Db 196 TCCATGGTGCTCACT 210

RESULT 5  
BF822715

LOCUS BF822715 321 bp mRNA linear EST 13-JAN-2001  
DEFINITION CM3-RT0006-091200-545-cl2 RT0006 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF822715  
VERSION BF822715.1 GI:12162929  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-RT0006->



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2003, 10:13:13 ; Search time 2294 Seconds  
(without alignments)  
158.922 Million cell updates/sec

Title: US-09-716-320-3  
Perfect score: 15  
Sequence: 1 tccatggtgtcact 15

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estinu:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_estfun:\*  
15: em\_estom:\*  
16: em\_gss\_hum:\*  
17: em\_gss\_inv:\*  
18: em\_gss\_pln:\*  
19: em\_gss\_vrt:\*  
20: em\_gss\_fun:\*  
21: em\_gss\_mam:\*  
22: em\_gss\_mus:\*  
23: em\_gss\_pro:\*  
24: em\_gss\_rrod:\*  
25: em\_gss\_phg:\*  
26: em\_gss\_vrl:\*  
27: gb\_gss1:\*  
28: gb\_gss2:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	173	14	W31091 zb86h07.r1
2	15	100.0	232	9	AW637280 bl56g11.w
3	15	100.0	268	9	AA360512 EST69742
4	15	100.0	269	10	BE132222 db43g01.y

5	15	100.0	321	10	BF822715
6	15	100.0	322	9	AI008593
7	15	100.0	329	12	BI042474
8	15	100.0	357	13	BY400016
9	15	100.0	379	9	AA085493
10	15	100.0	381	10	BG121876
11	15	100.0	389	10	AW886682
12	15	100.0	393	12	BI057614
13	15	100.0	398	28	BH096821
14	15	100.0	400	28	AQ296272
15	15	100.0	432	14	R32275
16	15	100.0	444	13	BY556459
17	15	100.0	459	9	AW636779
18	15	100.0	463	12	BM708050
19	15	100.0	470	9	AU243882
20	15	100.0	474	14	N31328
21	15	100.0	484	9	AA312237
22	15	100.0	512	9	AA452475
23	15	100.0	513	29	BZ873773
24	15	100.0	514	10	BE018291
25	15	100.0	521	12	BM823695
26	15	100.0	523	10	BE971148
27	15	100.0	524	10	BF875537
28	15	100.0	577	9	AL636508
29	15	100.0	594	13	BQ308056
30	15	100.0	604	9	AV714029
31	15	100.0	606	12	BJ029020
32	15	100.0	616	10	BE867032
33	15	100.0	666	12	BI891968
34	15	100.0	672	12	BM724884
35	15	100.0	679	29	AG103671
36	15	100.0	690	28	AZ733709
37	15	100.0	722	12	BI871769
38	15	100.0	731	10	BE793514
39	15	100.0	743	10	BF792458
40	15	100.0	747	14	CD511710
41	15	100.0	772	10	BE790912
42	15	100.0	776	9	AU132253
43	15	100.0	786	10	BG435979
44	15	100.0	789	10	BE799238
45	15	100.0	816	10	BG683112

ALIGNMENTS

RESULT 1	W31091	173 bp	linear	EST 20-AUG-1996
LOCUS	zb86h07.r1	Soares_senescent_fibroblasts_NbHSF	Homo sapiens	cdNA
DEFINITION	clone IMAGE:310525 5', mRNA sequence.			
ACCESSION	W31091			
VERSION	W31091.1	GI:1312081		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 173)			
AUTHORS	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.			
TITLE	Generation and analysis of 280,000 human expressed sequence tags			
JOURNAL	Genome Res. 6 (9), 807-828 (1996)			
MEDLINE	97044478			
PUBMED	8889549			
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800			

Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1238 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 64.

## FEATURES

Location/Qualifiers

1. 173  
/organism="Homo sapiens"  
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/note="Vector: pT7T3D (Pharmacia) with a modified  
polylinker V\_TYPE: phagemid; Site\_1: Not I; Site\_2: Eco RI  
; 1st strand cDNA was primed with a Not I - oligo(dt)  
primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCCGCAATTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo."

## BASE COUNT

43 a 33 c 48 g 49 t

## ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 173;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15

|||||

Db 93 TCCATGGTGCTCACT 107

## RESULT 2

AW637280

LOCUS

AW637280 232 bp mRNA linear EST 26-APR-2001  
bl56g11.w1 Blackshear/Soares normalized xenopus egg library xenopus  
laevis cDNA clone PBX0056G11 5', mRNA sequence.

AW637280

AW637280.1 GI:7394388

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 232)

Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.

Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman

,J.W., Bonaldo,M.F. and Soares,M.B.

The NIEHS Xenopus maternal EST project: interim analysis of the

first 13,879 ESTs from unfertilized eggs

Gene 267 (1), 71-87 (2001)

21211403

PUBMED

COMMENT

Contact: Perry J. Blackshear

Office of Clinical Research and Laboratory of Signal Transduction

National Institute of Environmental Health Sciences

A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,

USA

Tel: 919 541-4899

Fax: 919 541-4571

Email: black009niehs.nih.gov

Clone is available through Research Genetics, Inc., 2130 Memorial

parkway, Huntsville, AL 35901

phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email

cdnaeresgen.com

DNA Sequencing and analyses performed by National Institutes of  
Health Intramural Sequencing Center (NISC).

PCR Primers

FORWARD: TGTAACACGACGGCCAGT

BACKWARD: CAGGAACAGCTATGACC

Plate: 0056 row: G column: 11

Seq primer: T7 primer.

## FEATURES

Location/Qualifiers

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/lab\_host="DH10B"  
/clone\_lib="Blackshear/Soares normalized Xenopus egg  
library"  
/note="Vector: pT7T3-Pac; Site\_1: EcoRI; Site\_2: NotI;  
PolyA-selected mRNA was prepared from unfertilized Xenopus  
laevis eggs. The library was constructed in the vector  
pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and  
Soares, M.B. 'Normalization and subtraction: two  
approaches to facilitate gene discovery', Genome Research  
6:791-806, 1996. The first strand synthesis used a  
NotI-dt18 primer; double stranded cDNAs were ligated to  
EcoRI adapters, digested with NotI, and directionally  
cloned into the NotI and EcoRI-digested pT7T3-Pac vector.  
The library contained approximately 7.2 X 10<sup>4</sup>  
recombinants, with average insert sizes of 1-1.5 kb."

## BASE COUNT

71 a 49 c 65 g 47 t

## ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 232;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15

|||||

Db 67 TCCATGGTGCTCACT 81

## RESULT 3

AA360512

LOCUS

DEFINITION

AA360512 268 bp mRNA linear EST 21-APR-1997  
EST69742 T-cell lymphoma Homo sapiens cDNA 5' end similar to  
hereditary multiple exostoses gene 2 (EXT2), mRNA sequence.

AA360512

AA360512.1 GI:2012902

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 268)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Molero-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.

, Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,

Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,

Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon



M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280  
96026280  
MEDLINE  
PUBMED  
COMMENT  
Other\_ESTs: THC194116  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..268  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="AtCC (inhost):164695"  
/db\_xref="taxon:9606"  
/cell\_type="T-lymphocyte"  
/clone\_lib="T-cell lymphoma"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"

FEATURES  
source

BASE COUNT 67 a 46 c 77 g 76 t 2 others  
ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCATGGTGCTCACT 15  
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Db 248 TCCATGGTGCTCACT 262

RESULT 4  
BE132222  
LOCUS 269 bp mRNA linear EST 29-JUN-2000  
DEFINITION db43g01.y1 Blackshear/Soares normalized xenopus egg library Xenopus laevis cDNA clone IMAGE:3301296 5', mRNA sequence.  
ACCESSION BE132222  
VERSION BE132222.1 GI:8579587  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.  
AUTHORS 1 (bases 1 to 269)  
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.  
TITLE WashU Xenopus EST project, 1999  
JOURNAL Unpublished  
COMMENT Contact: Sandy Clifton, Ph.D.  
WashU Xenopus EST project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: [info@image.llnl.gov](mailto:info@image.llnl.gov)

FEATURES  
source

Seq primer: -40RP from Gibco  
High quality sequence stop: 268.  
Location/Qualifiers  
1..269  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:3301296"  
/sex="female"  
/tissue\_type="unfertilized egg"  
/cell\_type="unfertilized egg"  
/dev\_stage="unfertilized egg"  
/lab\_host="DH10B"  
/clone\_lib="Blackshear/Soares normalized Xenopus egg library"  
/note="Vector: pT7T3-Pac; Site\_1: EcoRI; Site\_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT7T3-Pac vector. The library contained approximately 7.2 X 10^5 recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 269;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCATGGTGCTCACT 15  
|||||  
Db 196 TCCATGGTGCTCACT.210

RESULT 5  
BF822715

LOCUS 321 bp mRNA linear EST 13-JAN-2001  
DEFINITION CM3-RT0006-091200-545-cl2 RT0006 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF822715  
VERSION BF822715.1 GI:12162929  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 321)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel.: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&tl2=CM3-RT0006->

091200-545-cl2&t3=2000-12-09&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 3  
High quality sequence stop: 321.

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Location/Qualifiers  
1. .321  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="RT0006"  
/note="Organ: kidney\_tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
88 a 63 c 88 g 82 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 321;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
|||||

Db 110 TCCATGGTGCTCACT 124

RESULT 6  
AI008593/c  
LOCUS  
DEFINITION  
EST203044 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone  
REMAZ48 3' end, mRNA sequence.  
AI008593  
ACCESSION  
AI008593.1 GI:3222425  
VERSION  
AI008593.1  
KEYWORDS  
EST.  
SOURCE  
Rattus sp.  
ORGANISM  
Rattus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
1 (bases 1 to 322)  
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,  
Kerlavage,A.R. and Adams,M.D.  
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat  
Gene Index  
Unpublished  
Contact: Lee, NH  
The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
Seq primer: M13-21.

FEATURES  
Location/Qualifiers  
1. .322  
/organism="Rattus sp."  
/mol\_type="mRNA"  
/db\_xref="ATCC (inhost):2016778"  
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/clone="REMAZ48"  
/dev\_stage="embryo 8, 12, 18 dpc"  
/clone\_lib="Normalized rat embryo, Bento Soares"  
/note="Vector: pT7T3pac; Site\_1: EcoRI; Site\_2: NotI"  
63 a 94 c 101 g 64 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
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Db 321 TCCATGGTGCTCACT 307

RESULT 7  
BI042474  
LOCUS  
DEFINITION  
RC5-OT0098-220101-011-C05 OT0098 Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
BI042474  
VERSION  
BI042474.1 GI:14449100  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 329)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-OT0098-  
220101-011-C05&t3=2001-01-22&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 82  
High quality sequence stop: 327.

FEATURES  
Location/Qualifiers  
1. .329  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="OT0098"  
/note="Organ: ovary; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
87 a 59 c 93 g 89 t 1 others

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 329;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
|||||

Db 285 TCCATGGTGCTCACT 299

RESULT 8  
BY400016/c  
LOCUS  
DEFINITION  
BY400016 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus



CDNA clone I730028H04 3', mRNA sequence.		Location/Qualifiers	
ACCESSION	BY400016	1..357	
VERSION	GI:26629584	/organism="Mus musculus"	
KEYWORDS	EST.	/mol_type="mRNA"	
SOURCE	Mus musculus (house mouse)	/strain="DBA/2"	
ORGANISM	Mus musculus	/db_xref="taxon:10090"	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 357)	/clone="I730028H04"	
AUTHORS	Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nixaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.	/cell_line="CRL-1722 L5178Y-R"	
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	/clone_lib="RIKEN full-length enriched, CRL-1722 L5178Y-R"	
JOURNAL	Nature 420, 563-573 (2002)	106 a 79 c 80 g 91 t 1 others	
MEDLINE	22354683	BASE COUNT	
PUBMED	12466851	ORIGIN	
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site ( <a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a> ) for further details.	Query Match 100.0%; Score 15; DB 13; Length 357; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY 1 TCCATGGTGCTCACT 15       Db 65 TCCATGGTGCTCACT 51	
RESULT 9		AA085493	
LOCUS		AA085493 379 bp mRNA linear EST 01-AUG-1997	
DEFINITION		zn44c07.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:550284 5' similar to TR:E229331 E229331 PROTEIN RESPONSIBLE FOR HEREDITARY MULTIPLE EXOSTOSIS. ;, mRNA sequence.	
ACCESSION		AA085493	
VERSION		AA085493.1 GI:1628769	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 379) Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478 8889549 Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. Insert Length: 1156 Std Error: 0.00 Seq primer: -28M13 rev2 from Amersham.	
TITLE		Location/Qualifiers	
JOURNAL		1..379	
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PUBMED		/mol_type="mRNA"	
COMMENT		/db_xref="GDB:3928802"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:550284"	
		/sex="female"	
		/dev_stage="HeLa S3 cell line"	
		/lab_host="SOLR (kanamycin resistant)"	
		/clone_lib="Stratagene HeLa cell s3 937216"	
		/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3 epithelioid carcinoma cells grown to semi-confluency without induction. Average insert size: 1.5 kb; Uni-ZAP XR vector. -5' adaptor sequence: 5' GAATTCGGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"	
BASE COUNT		108 a 88 c 92 g 91 t	



JOURNAL  
MEDLINE  
PUBMED  
COMMENT

sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-GN0175-  
090301-203-h02&t3=2001-03-09&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 10  
High quality sequence stop: 364.

FEATURES  
source

1. .393  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="GN0175"  
/note="Organ: placenta\_normal; Vector: puc18; Site\_1: SmaI  
; Site\_2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

BASE COUNT 112 a 103 c 79 g 99 t  
ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
|||||  
Db 81 TCCATGGTGCTCACT 67

RESULT 13  
BH096821/C  
LOCUS

DEFINITION  
BH096821 398 bp DNA linear GSS 19-JUL-2001  
RPCI-24-298D11.TJ RPCI-24 Mus musculus genomic clone RPCI-24-298D11  
, genomic survey sequence.

ACCESSION  
BH096821  
VERSION  
BH096821.1 GI:14918167  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 398)  
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,  
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,  
Russell,D., de Jong,P. and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-24  
Unpublished  
Other\_GSSs: RPCI-24-298D11.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-24. For BAC  
library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC  
Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html  
Plate: 298 row: D column: 11  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source

1. .398  
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/db\_xref="taxon:10090"  
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/cell\_type="Spleen/Brain"  
/clone\_lib="RPCI-24"  
/note="Vector: PTARBAC1; Site\_1: BamH1; Site\_2: BamH1;  
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The  
library was cloned in the PTARBAC1 cloning vector at the  
BamH1 sites using MboI partially digested male C57BL/6J  
DNA."

BASE COUNT 141 a 85 c 84 g 88 t  
ORIGIN

Query Match 100.0%; Score 15; DB 28; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGCTCACT 15  
|||||  
Db 250 TCCATGGTGCTCACT 236

RESULT 14  
AQ296272  
LOCUS

DEFINITION  
AQ296272 400 bp DNA linear GSS 15-DEC-1998  
HS\_2166\_B2\_MR\_D05 CIT Approved Human Genomic Sperm Library D Homo  
sapiens genomic clone Plate=2166 Col=10 Row=H, genomic survey  
sequence.

ACCESSION  
AQ296272  
VERSION  
AQ296272.1 GI:4010340  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 400)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.

REFERENCE  
AUTHORS  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2166 row: H column: 10  
Class: BAC ends  
High quality sequence stop: 400.

FEATURES  
source

1. .400  
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